



1600

## RAW SEQUENCE LISTING

DATE: 10/10/2002

PATENT APPLICATION: US/09/327,750E

TIME: 09:46:14

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\10102002\I327750E.raw

5 <110> APPLICANT: Sato, Taki-Aki  
 9 <120> TITLE OF INVENTION: GENE ENCODING NADE, P75NTR- ASSOCIATED CELL DEATH EXECUTOR  
 AND USES  
 10 THEREOF  
 14 <130> FILE REFERENCE: 0575/59131/JPW/AJM/HA  
 18 <140> CURRENT APPLICATION NUMBER: 09/327,750E  
 20 <141> CURRENT FILING DATE: 1999-06-07  
 24 <160> NUMBER OF SEQ ID NOS: 45  
 28 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

840 <210> SEQ ID NO: 35  
 842 <211> LENGTH: (117) 118 shown  
 844 <212> TYPE: PRT  
 846 <213> ORGANISM: Mouse  
 850 <400> SEQUENCE: 35  
 852 Met Ala Ser Lys Phe Lys Gln Val Ile Leu Asp Leu Thr Val Glu Lys Asp  
 853 1 5 10 15  
 855 Lys Lys Asp Lys Arg Gly Gly Lys Ala Ser Lys Gln Ser Glu Glu  
 E--> 856 20 20 25 25 30 30  
 858 Pro His His Leu Glu Glu Val Glu Asn Lys Lys Pro Gly Gly Asn Val  
 E--> 859 35 35 40 40 45 45  
 861 Arg Arg Lys Val Arg Arg Leu Val Pro Asn Phe Leu Trp Ala Ile Pro  
 E--> 862 50 55 60  
 864 Asn Arg His Val Asp Arg Asn Glu Gly Gly Glu Asp Val Gly Arg Phe  
 E--> 865 65 70 75 80  
 867 Val Val Gln Gly Thr Glu Val Lys Arg Lys Thr Thr Glu Gln Gln Val  
 E--> 868 85 90 95  
 870 Arg Pro Tyr Arg Arg Phe Arg Thr Pro Glu Pro Asp Asn His Tyr Asp  
 E--> 871 100 105 110  
 873 Phe Cys Leu Ile Pro  
 E--> 874 115  
 876 <210> SEQ ID NO: 36  
 878 <211> LENGTH: (110) 111  
 880 <212> TYPE: PRT  
 882 <213> ORGANISM: Mouse  
 886 <400> SEQUENCE: 36  
 888 Met Ala Asn Ile His Gln Glu Asn Glu Glu Met Glu Gln Pro Met Gln  
 889 1 5 10 15  
 891 Asn Gly Glu Glu Asp Arg Pro Leu Gly Gly Gly Glu Gly His Gln Pro  
 892 20 25 30  
 894 Ala Gly Asn Arg Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp

pp 1-3  
 Does Not Comply  
 Corrected Diskette Needed

Per 1.822 of  
 Sequence Rules,  
 a MAXIMUM of  
 16 amino acids  
 per line allowed  
 misaligned  
 amino acid  
 numbers - see  
 item 3 on Error  
 Summary Sheet

see p. 2

MAXIMUM  
 16 amino acids  
 per line

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```

895          35          40          45
897 Ala Ile Pro Asn Arg Gln Ile Asn Asp Gly Met Gly Gly Asp Gly Asp
E--> 898      50          55          60
900 Asp Met Glu Ile Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu
E--> 902 65          70          75          80
904 Arg Glu Leu Gln Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu Leu
E--> 905          85          90          95
907 Ser Asn His His Asp His His Asp Glu Phe Cys Leu Met Pro
E--> 908      100          105          110
910 <210> SEQ ID NO: 37
912 <211> LENGTH: 120
914 <212> TYPE: PRT
916 <213> ORGANISM: Mouse
920 <400> SEQUENCE: 37
922 Met Glu Gln Pro Leu Gln Asn Gly Gln Glu Asp Arg Pro Val Gly Gly
923 1          5          10          15
925 Gly Glu Gly His Gln Pro Ala Ala Ala Asn Asn Asn His Asn His Asn His
926          20          25          30
928 Asn His Asn His Ser His Asn His Asn His His Arg Arg Gly Gln
E--> 929      35 35          40 40          45 45
931 Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp Ala Ile Pro Asn Arg Gln
E--> 932      50          55          60
934 Met Asn Asp Gly Leu Gly Gly Asp Gly Asp Asp Met Glu Met Phe Met
E--> 936 65          70          75          80
937 Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg
E--> 938          85          90          95
940 Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn His His Asp His
E--> 941      100          105          110
943 His Asp Glu Phe Cys Leu Met Pro
E--> 944      115          120
946 <210> SEQ ID NO: 38
948 <211> LENGTH: (122)
950 <212> TYPE: PRT
952 <213> ORGANISM: Mouse
956 <400> SEQUENCE: 38
958 Met Ala Asn Val His Gln Glu Asn Glu Glu Met Glu Gln Pro Leu Gln
959 1          5          10          15
961 Asn Gly Gln Glu Asp Arg Pro Val Gly Gly Gly Glu Gly His Gln Pro
962          20          25          30
964 Ala Ala Asn Asn Asn Asn Asn His Asn His Asn His Asn His His Arg Arg
E--> 965      35          40          45
967 Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp Ala Ile Pro Asn
E--> 968      50          55          60
970 Arg Gln Met Asn Asp Gly Leu Gly Gly Asp Gly Asp Asp Met Glu Met
E--> 971 65          70          75          80
973 Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln
E--> 974          85          90          95
976 Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn His His
E--> 977      100          105          110

```

*misaligned  
nos.*

*16 per line*

*misaligned  
amino acid  
nos.*

*see p. 3*

*16 per line*

*misaligned  
nos.*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/327,750E

DATE: 10/10/2002  
TIME: 09:46:14

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF4\10102002\I327750E.raw

979 Asp His His Asp Glu Phe Cys Leu Met Pro  
E--> 980 115 120

*misaligned*

## VERIFICATION SUMMARY

DATE: 10/10/2002

PATENT APPLICATION: US/09/327,750E

TIME: 09:46:15

Input Set : A:\PTO.VSK.txt

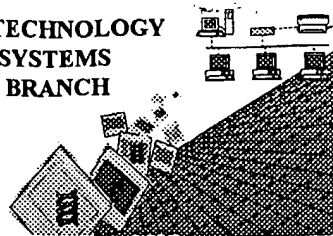
Output Set: N:\CRF4\10102002\I327750E.raw

L:145 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:856 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35  
M:332 Repeated in SeqNo=35  
L:874 M:252 E: No. of Seq. differs, <211> LENGTH:Input:117 Found:118 SEQ:35  
L:898 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36  
M:332 Repeated in SeqNo=36  
L:908 M:252 E: No. of Seq. differs, <211> LENGTH:Input:110 Found:111 SEQ:36  
L:929 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37  
M:332 Repeated in SeqNo=37  
L:965 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38  
M:332 Repeated in SeqNo=38  
L:980 M:252 E: No. of Seq. differs, <211> LENGTH:Input:122 Found:124 SEQ:38

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/327,750 E
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino _____ Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#26  
1634  
10/24/02  
RECEIVED

OCT 22 2002

TECH CENTER 1600/2900

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/327,750E  
Source: 1600  
Date Processed by STIC: 10/10/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002